Package ‘meshes’

March 28, 2024

Title  MeSH Enrichment and Semantic analyses
Version  1.28.0
Description  MeSH (Medical Subject Headings) is the NLM controlled vocabulary
used to manually index articles for MEDLINE/PubMed. MeSH terms were
associated by Entrez Gene ID by three methods, gendoo, gene2pubmed and RBBH.
This association is fundamental for enrichment and semantic analyses.
meshes supports enrichment analysis (over-representation and gene set
enrichment analysis) of gene list or whole expression profile.
The semantic comparisons of MeSH terms provide quantitative ways to compute
similarities between genes and gene groups. meshes implemented five methods
proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively and supports
more than 70 species.

Depends  R (>= 4.1.0)
Imports  AnnotationDbi, DOSE, enrichplot, GOSemSim, methods, utils,
        AnnotationHub, MeSHDbi, yulab.utils
Suggests  knitr, rmarkdown, prettydoc
VignetteBuilder  knitr
ByteCompile  true
License  Artistic-2.0
BugReports  https://github.com/GuangchuangYu/meshes/issues
biocViews  Annotation, Clustering, MultipleComparison, Software
Encoding  UTF-8
LazyData  true
RoxygenNote  7.1.2
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Repository  Bioconductor 3.18
Description

MeSH term enrichment analysis

Usage

enrichMeSH(
  gene,
  MeSHDb,
  database = "gendoo",
  category = "C",
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  qvalueCutoff = 0.2,
  minGSSize = 10,
  maxGSSize = 500,
  meshdbVersion = NULL
)

Arguments

gene a vector of entrez gene id
MeSHDb MeSHDb
database one of ’gendoo’, ’gene2pubmed’ or ’RBBH’
geneSim

pvalueCutoff Cutoff value of pvalue.
pAdjustMethod one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe background genes
qvalueCutoff qvalue cutoff
minGSSize minimal size of genes annotated by Ontology term for testing.
maxGSSize maximal size of genes annotated for testing
meshdbVersion version of MeSH.db. If NULL (the default), use the latest version.

Value
An enrichResult instance.

Author(s)
Guangchuang Yu

See Also
class?enrichResult

Examples

```
## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(a, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDb::MeSHDb(filepath_hsa)
data(geneList, package="DOSE")
de <- names(geneList)[1:100]
x <- enrichMeSH(de, MeSHDb = db, database='gendoo', category = 'C')

## End(Not run)
```

geneSim
geneSim

description
semantic similarity between two gene vector

Usage
geneSim(geneID1, geneID2 = NULL, measure = "Wang", combine = "BMA", semData)
Arguments

- geneID1: gene ID vector
- geneID2: gene ID vector
- measure: one of "Wang", "Resnik", "Rel", "Jiang" and "Lin"
- combine: One of "max", "avg", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple DO terms associated with gene/protein.
- semData: gene annotation data for semantic measurement

Value

score matrix

Author(s)

Guangchuang Yu

Examples

```r
## library(meshes)
## library(AnnotationHub)
## ah <- AnnotationHub()
## qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
## filepath_hsa <- qr_hsa[[1]]
## db <- MeSHDb::MeSHDb(filepath_hsa)
## hsamd <- meshdata(db, category="A", computeIC=T, database="gendoo")
data(hsamd)
geneSim("241", "251", semData=hsamd, measure="Wang", combine="BMA")
```

Description

Gene Set Enrichment Analysis of MeSH

Usage

```r
gseMeSH(
  geneList,
  MeSHDb,
  database = "gendoo",
  category = "C",
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  eps = 1e-10,
  pvalueCutoff = 0.05,
)```
gseMeSH

```r
pAdjustMethod = "BH",
verbose = TRUE,
seed = FALSE,
by = "fgsea",
meshdbVersion = NULL,
...
)
```

### Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>geneList</code></td>
<td>order ranked geneList</td>
</tr>
<tr>
<td><code>MeSHDb</code></td>
<td>MeSHDb</td>
</tr>
<tr>
<td><code>database</code></td>
<td>one of 'gendoo', 'gene2pubmed' or 'RBBH'</td>
</tr>
<tr>
<td><code>exponent</code></td>
<td>weight of each step</td>
</tr>
<tr>
<td><code>minGSSize</code></td>
<td>minimal size of each geneSet for analyzing</td>
</tr>
<tr>
<td><code>maxGSSize</code></td>
<td>maximal size of genes annotated for testing</td>
</tr>
<tr>
<td><code>eps</code></td>
<td>This parameter sets the boundary for calculating the p value.</td>
</tr>
<tr>
<td><code>pvalueCutoff</code></td>
<td>pvalue Cutoff</td>
</tr>
<tr>
<td><code>pAdjustMethod</code></td>
<td>pvalue adjustment method</td>
</tr>
<tr>
<td><code>verbose</code></td>
<td>print message or not</td>
</tr>
<tr>
<td><code>seed</code></td>
<td>logical</td>
</tr>
<tr>
<td><code>by</code></td>
<td>one of 'fgsea' or 'DOSE'</td>
</tr>
<tr>
<td><code>meshdbVersion</code></td>
<td>version of MeSH.db. If NULL (the default), use the latest version.</td>
</tr>
<tr>
<td><code>...</code></td>
<td>other parameter</td>
</tr>
</tbody>
</table>

### Value

gseaResult object

### Author(s)

Yu Guangchuang

### Examples

```r
## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDbi::MeSHDb(filepath_hsa)
data(geneList, package="DOSE")
y <- gseMeSH(geneList, MeSHDb = db, database = 'gene2pubmed', category = "G")

## End(Not run)
```
meshdata

Description

construct annoData for semantic measurement

Usage

meshdata(MeSHDb = NULL, database, category, computeIC = FALSE)

Arguments

MeSHDb MeSHDb package
database one of supported database
category one of supported category
computeIC logical value

Value

a GOSemSimDATA object

Author(s)

Guangchuang Yu

Examples

```r
## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDb::MeSHDb(filepath_hsa)
hsamd <- meshdata(db, category='A', computeIC=T, database="gendoo")
## End(Not run)
```
**Description**

Semantic similarity between two MeSH term vectors

**Usage**

meshSim(meshID1, meshID2, measure = "Wang", semData)

**Arguments**

- meshID1: MeSH term vector
- meshID2: MeSH term vector
- measure: one of "Wang", "Resnik", "Rel", "Jiang" and "Lin"
- semData: annotation data for semantic measurement, output by meshdata function

**Value**

Score matrix

**Author(s)**

Guangchuang Yu [https://guangchuangyu.github.io](https://guangchuangyu.github.io)

**Examples**

```r
## library(meshes)
## library(AnnotationHub)
## ah <- AnnotationHub()
## qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
## filepath_hsa <- qr_hsa[[1]]
## db <- MeSHDb::MeSHDb(filepath_hsa)
## hsamd <- meshdata(db, category='A', computeIC=T, database="gendoo")
## meshSim("D000009", "D009130", semData=hsamd, measure="Resnik")
```

**Description**

These datasets are used in meshes
| reexports | Objects exported from other packages |

**Description**

These objects are imported from other packages. Follow the links below to see their documentation.

- **DOSE** `geneID`, `geneInCategory`
- **enrichplot** `cnetplot`, `dotplot`, `emapplot`, `gseaplot`, `heatplot`, `ridgeplot`
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